

Fig. 1A

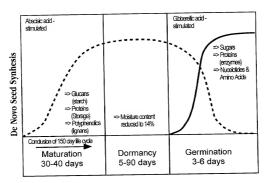


Fig. 1B

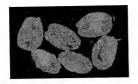


Fig. 1C



Fig. 1D



Fig. 1E



Fig. 1F

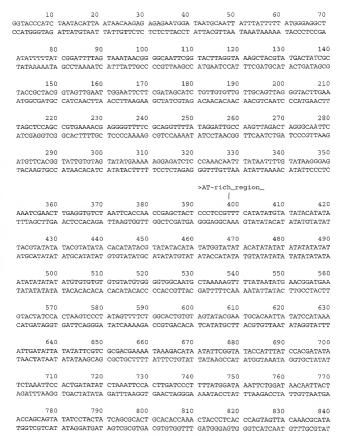


Fig. 2A

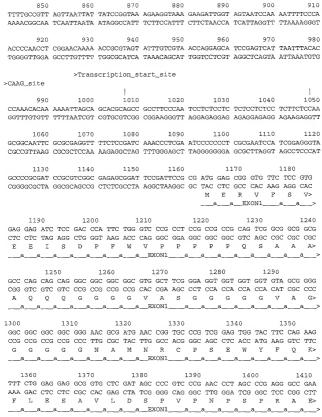


Fig. 2B

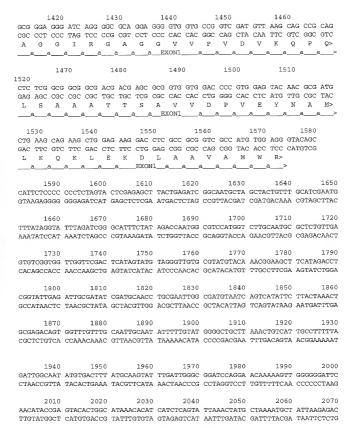


Fig. 2C

2080	2090	2100	2110	2120	2130	2140
CTTTAGCACC	TCTTATCTTA	TCAACCATGG	TGAAAAAATT	GAAGGGGGGA	CTCAGGGGGG	TATCCATGGG
GAAATCGTGG	AGAATAGAAT	AGTTGGTACC	ACTTTTTTAA	CTTCCCCCCT	GAGTCCCCCC	ATAGGTACCC
2150	2160	2170	2180	2190	2200	2210
TCCGATGGGT	GCAGGGGGGA	CTGAGTCCCC	CCTGCACCCA	CGTTGAATCC	GCCCTGGCAT	GCGTATAAGC
AGGCTACCCA	CGTCCCCCCT	GACTCAGGGG	GGACGTGGGT	GCAACTTAGG	CGGGACCGTA	CGCATATTCG
2220	2230	2240	2250	2260	2270	2280
TGTCACAGCC	ATTTCTAGGT	GCTTGTGCTT	AGTTGGGTGA	TGTCAGCTTA	ATTTGTCTTT	TCTATGTCGT
	TAAAGATCCA					
2290	2300	2310	2320	2330	2340	2350
CATCGATTT	CTAAGAAACG	AAAAATAGCC	TATTTATGTG	CTCCAGAATT	TGATGATCCC	TGGCCCTTCA
	GATTCTTTGC					
0111001111111	01111011100					
2360	2370	2380	2390	2400	2410	2420
	TTAGCCTATT				TATGTTGTTG	CAATGTGTGG
	AATCGGATAA					
AAACGACIII	Pricodilini	nomicomico	00121010141			
2430	2440	2450	2460	2470	2480	2490
	TTTTGTGCCC			TCATTTTTCT	ACATGACTTA	AAATGACACT
	AAAACACGGG					
GATACGGAGC	AAAACACGGG	AIAIIAAAIA	AIMMOOLIM	11011111111111	101110101111	
2500	2510	2520	2530	2540	2550	2560
	GCACTGATTG					
	CGTGACTAAC					
icicolidia	COTOMOTANO	CIMITIOGIAM	1111011111111	0111 0121011011		
2570	258	0 2	590	2600	2610	2620
	CATCTTCAG		ACA GTT CC	A CCT GAG C	GT CCT GGA	GCT GGT TCA
	GTAGAAGTC					
1110110 1111111	011101111010	A S G	T V P		R P G	A G S>
					_b_b_b	b b
263	0	2640	2650	2660	2670	2680
TCC TTG CT	G AAT GCA G	AT GTT TCA	CAC ATA GGC	GCT CCT AA	T TCC ATC G	GA GGTACTTA
	C TTA CGT C					
S L L		D V S	H I G	A P N		G>
	bbb					
			0112	~~~	_~~_	
2690	2700	2710	2720	2730	2740	2750
	TTACATTTTC					
	AATGTAAAAG					
AGAATAGACC	. AAIGIAAAAG	TOTACHATA	CILIGHIGG	LILININGGAC	01011MACG1	11CCC1AA111

Fig. 2D

2760	2770	2780	2790		2810	2820
				CACGTCATCA		
AAAATCAAAG	AAACTTTATC	TTCATCTCAA	CATAACGACA	GTGCAGTAGT	TTATCAAGAC	TTCGATACTT
2830	2840	2850	2860	2870	2880	2890
TAAATAAGTT	CCGCATTTGT	TAGTGATTCT	TTGAACATTA	GAATTGTTAT	GCTTAAGTAG	ATAGGGTTAT
				CTTAACAATA		
ATTIMITORN	GGCGIIIIIGI	112 0110 11 11 1011				
2900	2910	2920	2930	2940	2950	2960
				CCAGCTGGCA		
				GGTCGACCGT		
CAAACAAACC	TCAAGGGAAT	TIAGIAAAGI	AACGAC I GAC	. GGICGACCGI	CCICOIMMIC	THICH I COOL II
		2990	3000	3010	3020	3030
2970	2980					
				AAAACATATT		
CTGGTACTTA	CTTCTGGAAG	GACAAGACTC	ACGAGTGTTC	TTTTGTATAA	AACTAATTAC	GTGGAACTTA
3040	3050	3060	3070		3090	
				GAGTAGTACT		
GGAATCCTAG	AACGTTTCTA	CCCGTGAATC	GAAATCTTAA	CTCATCATGA	ATTTATCGAC	AACAATAGTA
3110	3120	3130	3140	3150	3160	3170
				ACTITTGACT		
CTAAACAGGA	CATCACTTTA	CAGCTGTTTT	GTCCTTACGA	A TGAAAACTGA	AGACTATAAA	GTACGGACCG
3180	3190	3200	323	LO	3220	3230
TTTACTTATG	CTCTGTTTGG	AACATGGGCA	CATATCA GO	C AAT GCT A	CT CCA GTT	CAA AAC ATG
				CG TTA CGA T		
					T P V	O N M>
				c c c	EXON3 c	cc>
			_			
3240	3250	3.2	60	3270	3280	3290
				TTG GTA CA	G AAT GTT G	AT GTC CTT
				C AAC CAT GI		
L S G		G G S	G S O			D V L>
			EXON3	c c c		c c >
cc	_cc_	cc	EXUNS	_cc		
220	^	3310	3320	3330	3340	
330						
				G CAG TCA GA		
				C GTC AGT CT		
V K Q		S S S	S R E			D M K>
cc_	_cc_	cc	EXON3	_ccc_	_ccc_	c>
3350	3360	3370	3380	339	-	3400
				I GCT GAT CA		
CCT CTT CG	A CTC TGG T	GA CCT TGA	CGT TCT GG	A CGA CTA GI	T TCT AAT G	
G E A	ET	T G T	A R P	A D Ç	R L	Q R>
cc_	_ccc	cc	EXON3 _c	_ccc_	_ccc_	c>

Fig. 2E

3410		3420		3430		3440			450			160		34	
AGGTGATC	ΑT	TCATTGCT	TC	CTTGTAAT	ΑT	AGATTCTG	TA	CATA	ATTA	ACC	TACCI	rcg	TC.	ATGCAT	GC
TCCACTAG	TA	AGTAACGA	AG	GAACATTA	TZ	TCTAAGAC	ΑT	GTAT:	TAAT	TGG	ATGGA	AGC	AG'	TACGTA	CG
		2.40		350	20	35	10		350	20		353	0		3540
348 ATGTGTCCT	50	349	/U					CACTE			COTAC				
TACACAGGA	'A	TTTTCACCI	LT.	AGCCCTTT	om.	GIIGGAII	10	CMC1:	A A CITY	20 0	CONTO	raar	Δ.	AGTCAA	AGGA
TACACAGGA	ΥT	AAAAGTGGA	1A	TCGGGAAA	J.I.	CAACCIAA	AG	GIGM	AAG1	AG C	CCAIC	.001			
355	50	356	50	351	70	35	80		35	90		360	0		3610
ATTGCATCG	iC.	ATATATGAT	rc	TTTTACCT	AC	CATATTAG	TT	CTCT	STGT	GC (CATACT	TCAC	T	GCTTAG	TGTC
TAACGTAGO	CG	TATATACTA	ΑG	AAAATGGA'	TG	GTATAATC	AA	GAGA	CACA	CG (TATG	AGTO	A:	CGAATC	ACAG
362	20	363		36			50		36			367			3680
TCGAGCAAC	ΞA	GAGGAATT'	ΓG	TATGGCTA'	тт	ACACGTAG	CA	CTTT	GCTC'	TC '	PACTTO	GTT1	ľΑ	TTGACA	TAAG
AGCTCGTTC	CT	CTCCTTAA	ΑC	ATACCGAT	AA	TGTGCATC	GΤ	GAAA	CGAG.	AG 2	ATGAAG	CAA	AΤ	AACTGT	ATTC
369	90	370		37			20		37			374			3750
CAATTTGG	ЗA	TGAATTAA	AΤ	CTGAGTTC	AC	ATCATATT	CC	TTAT	GTCA	CA A	AGTTT	CTG	AA.	ACCGA'I	TGTA
GTTAAACC	ст	ACTTAATT	ΓA	GACTCAAG	TG	TAGTATAA	.GG	AATA	CAGT	GT '	rcaaa(GAC'	ГT	TGGCTA	ACAT
									38			38:	10		3820
376		37		37			90				T A OFFICE			303000	
TCTAGTAT	CT	GGTTGATG	CA	CCCCCATC	TT	GGATTIGC	AA	ATCA	AAGT	TA	TACTO	CCI	NG TO	momoc:	A A DC
AGATCATA	GΑ	CCAACTAC	GT	GGGGGTAG	AA	CCTAAACG	TT	TAGT	TTCA	AT.	ATGAG	GGA	ıc	101002	MAIG
38:	3 0	38	40	38	50	38	60		38	70		38	80		3890
COMPONENTS.	22	GCAATTAC				CGGATTTC	AT	AGCT	ATTG	AC '	TATGA	TTA	CC	AGAATT	CATT
CARACTAT	uu.	CGTTAATG	GG.	GTTATTTG	GT	GCCTAAAC	TA	TCGA	TAAC	TG .	ATACT:	AAT	GG	TCTTA	AGTAA
0/11/101111		00111111													
39	00	39			20		30			40		39			3960
TGGCAGCT.	ΑТ	TTTCTCAA	тт	TAAGTTTG	GT	ATTAGTCT	CA	GTTG	GCTG	TA	AAATA	ATG	TC	ACGGT	AGGGT
ACCGTCGA	TA	AAAGAGTT	AΑ	ATTCAAAC	CA	TAATCAGA	AGT	CAAC	CGAC	AT	TTTAT	TAC	AG	TGCCA?	rccca
39	70	39			90		000			10		40			4030
ACATGTAT	GT	GCAGCATA	.CA	AGGTATGG	GT	GAGTTATO	SAT	ATGG	ACAG	TG	TGTAC	ACC	CC	ACATT.	rgere
TGTACATA	CA	CGTCGTAT	ĠΤ	TCCATACO	CA	CTCAATA	CTA	TACC	TGTC	AC	ACATG	TGG	GG	TGTAA	ACGAG
						. 40	070		4.0	080		40	90		4100
	40		50		60						N M N C C		-	CDCD/CDCD/CD	
ACTAAAAT	'CA	AAATATTC TTTATAAG	AA.	ACGTCACG	FIG	ATGATAT	3GT	GGAT	TGCF	711	MINCO	ממני	77	AACAA:	TALIA
TGATTTTA	GT.	TTTATAAG	тт	TGCAGTGC	AC	TACTATA	JCA	CCIP	MCG	LAM	IMIGG	mac	PA I	Ancari	
4.1	10	41	20	41	130	4	140		4	L50		41	60		4170
		GCTAGACA							TTT	rgr	ATGAA	GAT	GT	TGAGC	AAGCA
ACAATCAA	CA	CGATCTGT	עדים.	TTATATCO	GA	CAAGAAA	ACC	CACI	CAAA	ACA	TACTI	CTA	CA	ACTCG	TTCGT
ACARIGAA	LCP3	CGAICIGI	. 16	IIMIMICO											
	.80		.90		200			10			220			4230	
CTTCTCGA	TA	TAATGCTA	GT	TTTGTTG	ACC	TGTTCC .	AGG	AAG	CAA	TCC	AAT	CGG	G.	AG TCA	GCC
GAAGAGCT	'nΤ	ATTACGAT	CA	AAACAAC!	rgo	ACAAGG '	TCC	TTC	GTT	AGG	TTA	GCC	C	TC AGT	CGG
							R	K	Q	S	N	R		E S	A>
								dc	E	dE	EXON4_		_d_	d	d>

Fig. 2F

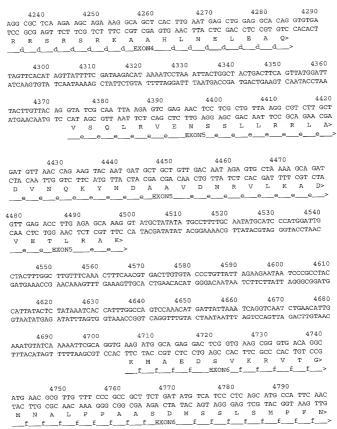


Fig. 2G

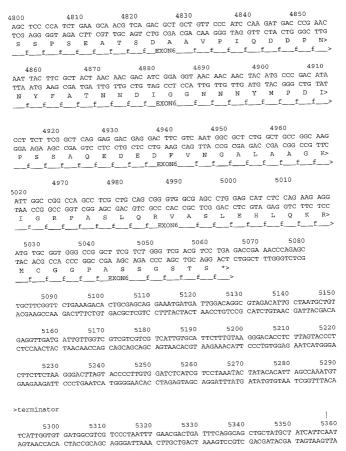


Fig. 2H

5370	5380	5390	5400	5410	5420	5430
AATATTTTGA	TCGATGCTTC	CTCTTGTCTT	TTGCTCTTAA	GCAACCAAGC	ATAAAGATAT	CACTACCTTT
TTATAAAACT	AGCTACGAAG	GAGAACAGAA	AACGAGAATT	CGTTGGTTCG	TATTTCTATA	GTGATGGAAA
5440	5450	5460	5470	5480	5490	5500
TGAGCTGTTC	ATTTGAAGTG	CAAAGCTAAG	CTCAATATCT	CAGGTGTTCA	TTTGAAGTTT	AAAGGTGAAC
ACTCGACAAG	TAAACTTCAC	GTTTCGATTC	GAGTTATAGA	GTCCACAAGT	AAACTTCAAA	TITCCACTIG
			5540	5550	5560	5570
5510	5520	5530	5540		TACATGTCAT	
TGATAACAAA	CGTCAGGCTA	TGGTGAATGA	TCCCTCCACA	TOTAGGGATT	ATGTACAGTA	AAAGTATTAG
ACTATIGTT	GCAGTCCGAT	ACCACIINCI	ICCCIGCACA	101110001111		
5580	5590	5600	5610	5620	5630	5640
STTDATTAGA	ATGCATTTTC		CCATCACAGT	TCATCATACA	AGCAAGTGTA	GTTATTAATG
TTTAATCAAC	TACGTAAAAG	TGGGTCTTAG	GGTAGTGTCA	AGTAGTATGT	TCGTTCACAT	CAATAATTAC
5650	5660	5670	5680	5690	5700	5710
GTAAATTTTT	CGTTTAGAGA	AAAAAAAAGG	AAGCCTTATA	TAAGATTCAC	CGGTGGGGTG	TGAACAATAA
CATTTAAAAA	GCAAATCTCT	${\tt TTTTTTTTCC}$	TTCGGAATAT	ATTCTAAGTG	GCCACCCCAC	ACTTGTTATT
					5770	5780
5720	5730	5740	5750			
TCAATGAATG	AGATCGCATC	CCGTAAGGGC	AGCCTAGCTA	GACAAAAATG	CATAAAACTC GTATTTTGAG	CCATATCCTT
AGTTACTTAC	TCTAGCGTAG	GGCATTCCCG	TCGGATCGAT	CIGITITIAC	GIMITITIGAG	GCAINIGGII
5790	5800	5810	5820	5830	5840	5850
2/90	CCTTCCCCAC	GCGCTCAAAT			CGCGGGCAAG	AAACGAATCA
CCACAACAAC	CGAACGCGTG	CGCGAGTTTA	CCGTCGCTGA	AGTAGCGAAA	GCGCCCGTTC	TTTGCTTAGT
0010110110	0012101111					
5860	5870	5880				5920
AGTGATACAT	TGGCAGGGAA	CCACCAAAAG	AAGGCCATCC	AATCCAATCC	ACTCCAACGC	GGCATGGAAG
TCACTATGTA	ACCGTCCCTT	GGTGGTTTTC	TTCCGGTAGG	TTAGGTTAGG	TGAGGTTGCG	CCGTACCTTC
					5980	5990
5930	5940	5950				
ACAAGACAGA	TGATTCACAG	CTATCTTCTG	CTTCTACAAG	TTIGATACTI	TGTACTGTCC	A A A CTCCCTT
TGTTCTGTCT	ACTAAGTGTC	GATAGAAGAC	GAAGATGTTC	AAACTATGAA	ACATGACAGG	AMAGICCCII
6000	6010	6020	6030	6040	6050	6060
777777777	CAGATTAGTC				GATCTTGTTG	TGGAGTGGCA
THTTTCTCCT	GTCTAATCAG	ACTAGAGCCC	GCGCAACTCA	AGAACACCCT	CTAGAACAAC	ACCTCACCGT
1111010011	. 010111110110					
6070						
GGAGTGACGA	TCGGCTGCCC	CGTTTTCTTC	TACCGAAACA	TCGCCAGTA	. AGAAGCCAAA	AAGACAATAA
CCTCACTGCT	AGCCGACGG	GCAAAAGAAG	ATGGCTTTGT	AGCGGTCATT	TCTTCGGTTI	TTCTGTTATT
			_			6200
6140						
TACGGCAATO	GGGATCGCCC	ATCTGCATAA	AACATTGCAT	GACGGAACTC	MITAATACAA	GAATGACATG CTTACTGTAC
ATGCCGTTAC	CCCTAGCGGG	TAGACGTATI	· TIGIAACGIA	A CTGCCTTGAC	. IAMITATGIT	CITACIGIAC
6210	6220	1				
	ATTACGCGT					
	TAATGCGCAG					

Fig. 2I

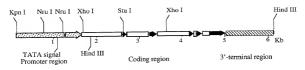


Fig. 3

TGATATGTGG GCCATGTGGC	160 170 180 TTATTTTCG GATCGAATT GCCACGTAAGC		250 260 270 CCAAAACC ACCATCCAAA CCGCCGAGGG	350 360 CAAATTTGTT GACAAGTTAA	440 450 CTCAAATTAA AGGGCCTTTT	530 540 PACACAC ATTITCTGCA	610 620 630 TACATCCATT AATCTTTTAT CAGAGGCAAA	710 720 ACCCAAC ACCAAGAAA	800 810 CTCTTTT TCCAACCGAT	890 900 CCTATAAAAC CCCATCCGAT	970 980 990 CTTCTAGTGA ITGTCTGATT GATCATCAAT	1060		
AA TGAT	160 TCG GATC		250 ACC ACCA	340 AAT CAA		520 CGC AGTI	610 ATT AATC	700 GAA ATT	790 CTC TTG		970 TGA ITG			
Secondary >Reb_site1	1 PPATTTT			3 GGACGAAA	4 TCCAATCC	CAACATGO	TACATCC	AACTTCA(CATTGTA	CCACAAA	CTTCTAG	1050		
AAGAAGAGGA .<	150 ATGAGAATTA	>reb_site2	240 CGCCACGTCAG	330 TTCGATTGAA GGACGAAAAT	390 400 410 420 430 TCCATTICAR ARATICIGI GAGCCATATA TCCGTGGGCT TCCAATCTC	500 510 520 530 ACABABACTAC TACCABCAGG CAACATGGGC AGTTACAGAC	600 TTAGTGTAGA	660 670 680 690 710 710 CAAAAATAGG TGACAAAA GTGTTATCTG CCACATACAT AACTTCAGAA ATTACCCAAC	780 790 800 CICITITGCAG CALTGIACIC INGCICITIT	870 ACAACCATGG	920 930 930 940 950 960 TCATCATCACA ACATATACA	1040		
AGAGAGGAGG	130 140 150 GAAACTGACA TGTGGGTCCC ATGAGAATTA	>Reb_site1 >re	230 AGCCACGTAAG	320 TATCTGGTTT	410 GAGCCATATA	500 ACAAAACTAC	590 GACAATCTCA	680 GTGTTATCTG	770 ACCTTTTTCA	860 CACCGTGCAC	950 GAGGAAAAAA	1030		Fig. 4
AGAGATGGTG	130 GAAACTGACA	>Reb	220 GAGTCAAATT	300 GATAGTTGAG GGACCCGTTG	400 AATATTCTGT	490 CCATAAAAGT	580 TTATCCCTAG	670 TGACACAAAA	760 AATCTTGGAA	850 ACACGAAGCT	940 ACAAACAAAA		ite	Ä
AGGAGAGGGG	120 TYCTTTTGTT		210 GATGAAGACC	300 GATAGTTGAG	390 TCCATTTCAA	480 TTTCAGTCAC	570 GAGCTAAGAG		750 GCAAGCTCCA	840 TACTTGATCT	930 TTCATCACCA	1020	Gus Star	
GCCTGCAGGG	110 120 CCCCACCATT TTTAATTCA TTCTTTTGTT		190 220 220 SCTACGTCA GATGAAGACC GAGTCAAATT	290 CACTGGTTTT	370 3GGACCTTAA ATGAACTTAT	460 470 TAAAATAGAT AATTGCCTTC	550 560 570 CATTICCACC ACGICACAA GAGCIAAGAG ITALCCIAG	650 CTCTTTATGA	730 760 AAATAAAAAA AAATCTTTTT GGAAGCTCCA AATCTTGGAA	830 CTCAAGCTTC		1010	CTAGAGGATC CCCGGGTGGT CAGICCCTT ALG Gus Start s	
AAGCTTGCAT GCCTGCAGGG AGGAGAGGGG AGAGATGGTG AGAGAGGAGG AAGAAGAGGA GGGGTGACAA	100 CCCCACCATT		190 GCTACGTCAA	280 ACCTCATCTG	370 GGGACCTTAA	460 TAAAATAGAT	550 CATTTCCACC	640 CGTAAAGCCG	730 AAATAAAAA	820 CCATGTCACC	910 CGCCATCATC	1000	CTAGAGGATC	

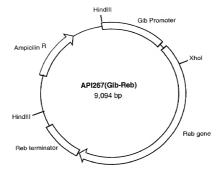


Fig. 5A

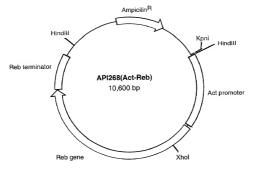
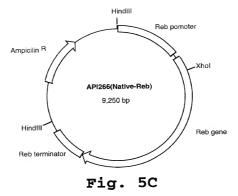
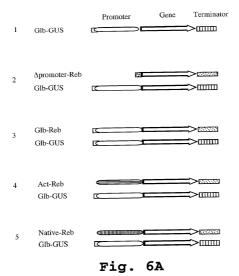


Fig. 5B





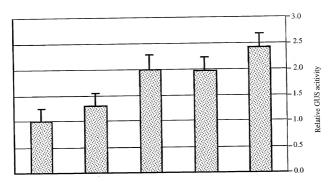


Fig. 6B

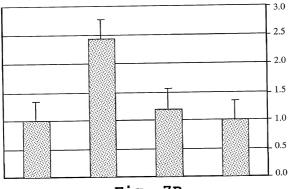




3 Glb Δ UAS-GUS

4 Native-Reb SIDAUAS-GUS SIDAUAS-GUS

Fig. 7A



Relative activity

Fig. 7B

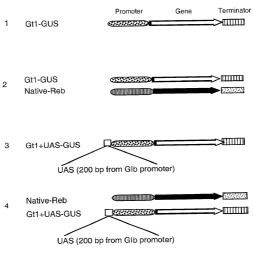
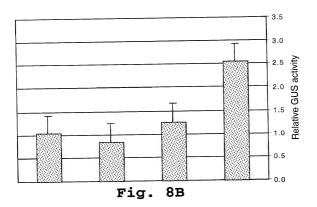


Fig. 8A



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| A DEPARTMENT A DEPARTMENT OF THE PROPERTY OF T | ACHGGGGCAGTTACAACATTTTCTGCACATTTTCCACAGGGCACAAAAAGGTTAAAGGTTATACCCTAGGGACAAAAAGTTTATCCCAAGGACATACAT | AGGT core AGGT core AGGT CONTINUED | IGITACACACATTTTCTCCACATCACAGGGTACAAAAGAGTAACAAGAGTATACAGATTATACCATAGAACATTTTCTCCACAGGGTACAAAAGAGTTATCCCAGAACATTACCATAACTTCAGCAAAAGAGTATACCCAAAAGAGTATACCCAAAAAGAGTATACCCAAAAAAAA | IGITACACACATTTTCTCCACATCACAGGGTACAAAAGAGTAACAAGAGTATACAGATTATACCATAGAACATTTTCTCCACAGGGTACAAAAGAGTTATCCCAGAACATTACCATAACTTCAGCAAAAGAGTATACCCAAAAGAGTATACCCAAAAAGAGTATACCCAAAAAAAA | IGITACACACATITICTCCACATCACACAGGGTACAAAAGAGTAACAGAGTATACAGATATATACACATATTCCACACACA | IGTRACACACTITICCACACTACACAGGGTACAAAAGAGTATACACTAGAGAGTATACACTAGAGACTATACTAGAGATATACTAGAGATATACTAGAGAGTATACACATACTAGAGAGTATACAGAGAGTATACACTAGAGAGTATACTAGAAAATACTAGAAAATACACAAAAAAAA
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 | ACHGGGGCAGTTACACACATTTTCTGCACATTTTCCACAGGGCACAAAAAAGAGTTAACACAAAAAATTACACAAAAAAAA | ACHGGGGAGTTACACACATTTYCTGCACATTTYCTCCACAGGGCAAAAAAAGGTTAACACATAACAGATTATTCCAACAGATTTYCTGCACACAGGGCACAAAAAAAGGTTAACACATACATACA | ACHIGGGCAGITACACACATITYCTGCACATTTYCTACACAGGGCACAAAAAAGGTAAGGGTATACACAGGACAALALAAAAAAATTTCTACACAAAAAAAAAA | ACHTGGGGCAGTTACAAAATTTTCTGCACATTTTCCACGGGTCACAAAGAGGTTATCCCTAGGACATACTATACATATTTCTGCACACGAGGTCACAAAGAGGTTATCCCTAGGACATACTTTATCCAAAGAGTTTATCCCTAGGACATACAT | ACHGGGGCAGTTACACACATTTTCTGCACATTTTCCACAGGTCACAAAGAGGTAAGAGTTATCCCTAGGACATACTTTTCACAACATTTTCTCACACACA
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ACHGGGGCAGTTACAAAATTTTCTGCACATTTTCCACAGGGCACAAAAAAGGGTTATCCCTAGGACATTCTALIAGATTTTCTAGAACATTTTCTAGAACATTTTCTAGAACATTTTCTAGAACATTAGAAAATTACCCAAAAGATTATTTTTTTT | ACHGGGGCAGTTACACACTTTTCTGCACATTTTCCACCACGTCACAAAAAGTTAAAGTTATACCCTAGGACACATTTTCTGCACAAAAATTACACATTTTCTGCACAAAAATTATAAAAAAAA | ACHIGGGCAGTTACACATTTTCTGCACTTTTCTACACAGAGGTAAGAGTTATCCTTTATCCTAGGAGTTATCCTTTATCCTAAGAGGTTATCCTTTATCCTAAGAGGTTATCCTTTATCCTAAGAGGTTATCTTTTTATCCTAAAATTACCCAACATTTTTTATCCTAAAAATTACCCAACATTTTTT | ACHGGGGAGTTACACACATTTYCTGCACATTTYCTACACGGGGCAAAAAAAAGGTAAAGGTTATUCUCTAGGACACATTCAALING ALINGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | ACHGGGGCAGTTACACACTTTTCTACACG <u>AGGT</u> CACAAAAAGAGTAAGAGTTATUCUCTAGGACACATULUALING INTERIALACACATUTTACACACATTTTCTACACACATTTTCTACACACAAAAAGGTAAAAAATTACCAAAAAGTTACACAAAAATTTATTATTATATAAAAAAAA
 | ACHGCGCAGITACACACATITTCTGCACATITTCTACACAGAGGCAAAAAGAGTAAGAGITATCUCUAGGACALTLULAIINGIA INAGALAIAAAAAAGAGGCGCAAAAAAAAAAGAGGCAAAAAATTACCAAAAAATTACCAAAAAATTACCCAAAAAGAGAAAATTATTACCAAAAAATTACCCAAAAAATTACCCAAAAAA | ACHGGGGCAGTTACACACATTTYCTGCACATTTYCTACACAGGTCACAAAGAGGTAAAGAGTTATUCUTAGGACATT.CA.LIAGAATTTYCTGCACAGGGCACAAAGAGGTTATUCUTAGGACATLCA.LIAGAATTTACAGAAAGAGGTAAAAAAGAAGAGGTAAAAAAAA | ACHGGGGCAGTTACACACATTTYCTGCACACTTTTCCACCACGTCACAAAGAGTTAAGAGTTATCCCTAGGACAAAATACTTATTACCAACACATTATCCTACAACATTTTCCTACAACA | ACHIGGGCAGITACACACITITYCTGCACATITTYCTACACAGGCAAAAAAGTTAAAAGTTAATACCAAGAAATACTTAAAAAGTTAAAAAAAA | ACHIGGGCAGITACACACITITYCTGCACATTTTCCACCACGICACAAAGAGGTAAGAGTTATUCUCIAGGACACATTTTCTGCACTACATTTTCCACCACGAGGCACATTTTCCACACGAGGCACATTTTCACACGAGGCACATTGCACAAAGTTTTATCACAAGGCACATACAT
 | ACHIGGGCAGITACACACATITYCTGCACATATTGCACCAGGTCACAAAGAGGTAAGAGTTATUCUTAGGACATATTTCTACACAGGTCACAAAGAGGTAAGAGTTATUCUTAGGACATATTTCTACACACAGGTCACAAAGGTAAGAGTTATTCCAGAAAGTTACCAAAAGTTATTCAGAGGCGTAAAAGTTACCCAAAAGTTATTCAGAAAATTACCCAAAAAGTTATTCTGCCACATAAATTACCCAAAAAGTTATTCTGCCACATAAATTACCCAAAAACTTATTATTCAGAAAATTACCCAAAAAAGTTATTCTGCCACATAAATTACCCAAAAACTTATATACAAAAAAAA | ACHIGGGCAGITACACACATITYCTGCACATITYTGCACCAGGGCACAAAAAAAGAGTAAAAAAITTATUCUAGGACAATITYCTTATATCCAACAAAAAAAAAAAAAAAAAAAA | ACHIGGGGCAGITACACACATITTCOACC <u>AGGG</u> CACAAAGAGGTAAGAGTTATCCUAGGACAALLICAIING I INGALACACACACACAGGCGCGCGCAAAAGAGGCCAAAAGAGGCCACATTATGACAAAAATAGGCAAAAGGCCGCTTTATGACAAAATAGGCAAAAGGTGACAAAAAGTTACCCAACACACAC | ACATGCGCAGTTACACACATTTTCTACCACGGGTCACAAAGAGGGTTATCCCTAGGACAAAAGAGGTTATCCCTAGGACATATTTCTACACCACGGGTCACAAAAGAGGTTATCCCTAGGACATTTTCTACACGGGTCACAAAAGAGGTCACAAAAAGAGGTCACAAAAAATTACCCAACACATAAAAAAAA | ACATGCGCAGTTACACACATTTCTCACC <u>ACGTCACAAAGAGCTAAAGAGTTATCCCTAGGACAATTTCCACCACGTCACAAAGAGGCTAAAGAGTTATCCCTAGGACATTTCCACCACGCTCACAAAGAGGTCACAAAGGTTATCCCTAGGAAATTTATCACAAAAGGTAAAAGCGTAAAAATTACCCAACACATACAT</u>
 | ACATGCGCAGTTACACACATTTTCTACACCACGTCACAAAGAGGTAAGAGTTATUCUTAGGACAALATULUAITAGLATAAAAAAAAAGAGGCAGTTATUCUTAGGACAATTTTCTACACACATTTCTACACACATTTTCTACAAAAATTACACAAAAATTACACAAAAAA | ACHIGGGCAGITACACACATITICTGCACATITICACACAGGTCACAAAGAGGTAAGAGGTTATUCUAGGACAALATATUCAAGAGAGTTATUCAAGAAAAAATACAGAGAGGACACAAAAAAGGGAAAAAAAGGCGCACATACAT | ACHTGGGGCAGTTACACACATTTTCTGCACATGGGCACAAAGAGGTAAGAGTTATUCUAGGACAALAGATTTTCTACACACACAGGGCACAAAGAGGTTATUCUAGGACAALAGATTTTCTACACACACAGGGCACATAAAGATTACCAAAAGATTACCCAAAAGATTACCCAAAAAGTTATTATCACAAAAGATTACCCAAAAAATTAGACAAAAAAAGATTATTATCACAAAAAAAA | ACHIGGGCAGITACACACATITYCTGCACATTTYCOACC <u>AGGIC</u> ACAAAGAGGTAAGAGTATACUCUAGGACACATL LUALING LIBALACATATACACACATACATACACACACACACACAGAGGTAACACAAAAGGTAACACAAAAGGTAAAAATTACACAAAAAGGTAAAAAAAGGTAACAAAAAAAA | ACHIGGGGAGITACACACATITYCTGCACATTTTGCACC <u>AGGG</u> CACAAAGAGGTAAGAGTATUCUTGGACACATULUAIDAGA GAGATTTTGCACCAGGGGCAAAGAGGCGCAAAGAGGCGCACATTTACAAAAATTACCCAAAAATTACCCAACACACACACACACACACACACACACACACACACA
 | ACHTGCGCAGTTACACACATTTTCTACCACC <u>ACGT</u> CACAAAGAGTAAGAGTTATCCTAGGACATTTTCTACCACCACGTTCTCTAGGACATTTTCTACACGTAGGAGTTAAGGAGTTAAGGAGTACCTAAAGAGAGAG | ACATGGGGCAGTTACACATTTTCTACCACG <u>CGT</u> CACAAAGAGTTAAGAGTTATCCTCTAGGACATTTCCACCACGTCACAAAGAGTTATCCTAGGACATTTTCTAGGACTTAGGATTTTCTAGGAGGAGTTAAGATTACACATTAGGAGGAAAGTTACAAGAGGTAAAAAAGTGTTAACAGAGAGAAAAATTAACAAAAAAGTGTTAATAAAAAAAGTGTTAACAAAAAAAA | ACATGGGGCAGTTACACATTTTCTACCACG <u>CGT</u> CACAAAGAGTTAAGAGTTATCCACATAGATTTTCTACACGTTATACAGGTTATCCACGAGTTAAGAGTTAACATTTTCTACACGAGTTATCCACACATTTTCTACACGAAATTTCTACACACATAAATTAACACACAC | ACATGCGCGCAGTTACACATTTCCACC <u>ACGT</u> CACAAAGAGCTAAAGAGTTAACCCTAGGACAATTTCCACC <u>ACGT</u> CACAAAGAGTTAACCCTAGGACAATTTCCACCACGCGCGCG | ACATGCGCGAGTTACACAATTTTCTGCACATTTTCCACC <u>ACGT</u> CACAAAGAGTTAAGAGTTATCCTCCTAGGACAATTTTCTACACACATTTTCCACC <u>ACGT</u> CACAAAGAGTTAACACATTATCACACACATTATCACACACA
 | ACATGGGGGAGTTACACACATTTTCTGCACATTTCCACC <u>ACGG</u> CACAAAGAGGTAAGAGTTATACAGGTTATCCACACATTTTCCACCA <u>CGGG</u> CACAAAGAGGTAAAGAGTTATACACATTATACACACACAC | ACATGGGGCAGTTACACATTTTCTGCACATTTTCCACCAGGGCAAAAAAAGAGTTAAUUUUTAGGAAAAATTULAAIINALAIAAAAAAAGTTAAUUUUAGGAAAAATTULAAIINALAIAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | ACATGCGCAGTTACACATTTTCTGCACATTTTCCACCAGGCAAAAAAAA | ACATGGGGCAGTTTTCTGCAGATTTCCACCAGGTCACAAAGAAGTTAACAAGTTATCCTGCAGGTCACAAAGAAGTTATCCTGCAGAATTTCCACCAGGTCACACAAGAAGTTAACAAGAAGTTAATCCTACAAAAAGTTAATCCTACAAAAATTCCACAAAAATTACCCAAAAACAAC | ACHTGCGCAGFTACACATTTTCTGCACCACTGCGCAAAAAAGAGTTAAAAGAGTTATCCACCAGGGCAAAAGAGTTATACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA
 | ACATGGGGGAGTTACACACATTTTCTGCACG <u>CGT</u> CACAAAGAGGTAAAGAGTTATUCUCTAGGACAAATTTTCTGCACG <u>CGT</u> CACAAAGAGGTTATUCUCTAGGACAAATTTTCTACGCACG <u>CGT</u> CACAAAGAGGTTATUCUCTAGGACAAAAAAAGAGTTATUCUCTAGGACAAAAAAAAGAGGTTATUCCTAGGACAAAAAAAGAGGTTATUCCTAGGACAAAAAAAAAA | ACATGGGGGAGTTACAGGAATTTCGGCAATTTCGACG <u>CGGGG</u> CACAAAGAGAGTAACAAGTTATCCTAGAATTTTCGACGAATTTCCACGAATTTCCACGAATTTCCACGAATTTCCACGAATTTCCACGAATTTCCACGAATTTCACACGAATTTCACACGAATTTCACACGAATTTCACACGAATTTCACACGAATTTCACACGAATTTCACACGAATTTCACACGAATTTCACACGAATTTCACACGAATTTCACACACGAATTTCACACACA | ACATGCGCAGTTACACATTTTCTGCACATTTCCACCAGGTCACAAAAAGTTAACAAGTTAACCAAGAAAAAAATTAAAAAAAA | ACATGCGCAGTTTCTCCACATTTCCACCAGTTTCCACCAGGTCACAAAAAGAGTTAATCCTAGAAGAGTTAATCCAAAAAAAA | ACATGGGGCAGTTACCACATTTTCCACCA <u>CGT</u> CACAAAGAGTAALUCCTAGGACAATTTCTACACATTTTCCACCA <u>CGT</u> CACAAAGAGTTAALUCCTAGGACAATTTTCTACACATTTTCTACACATTTTCTACACAATTTTTCTACACAATTTTTT
 | ACATGGGGCAGTTACCACATTTTCTGCACATTTTCCACC <u>ACGT</u> CACAAGAGTTAACAAGAGTTATUCCTAGGACAATUTUATTAGTGATAAAAGAGTTATUCCTAGGACAATTTTCTGCACATTTTCTACCACAAGAGTTAATGAGAAAAGAGATAAUCCTAGGACAATUTUATTAGTGATAAAAAAGAGATAAAAAAAAAA | ACATGGGGCAGTTACACACATTTCCGCACATTTCCACC <u>ACGG</u> CACAAAGAGTAACAAGTTATCCTACACATTTTCTGCACATTTTCTGCACATTTTCTACACCATTTTCTACACCATTTTCTACACAACA | ACATGCGCGGFTACACACATTTCTGCACACATTTCCACC <u>ACGT</u> CACAAAGAGGTAAAGAGFTATCCTGAGGACAATTTCTAGAGATTTCCACCACAGGAGAGAGA | ACHIGGGCAGITACACACATITIVETGCACATITTCCACC <u>ACGT</u> CACAAAGAGCIAAGAGITATUCCIAGGACAALULUALIAGAGAAGAATATACACCAGATATACACACATITTCACCAGATATACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAAGA | ACATGGGGGAGTTACACACATTTTCTCCACC <u>ACGT</u> CACAAAGAACTAAGAAGTTATUCCTAGGACAALLILAILINGI
GUINGALAAACAAGTTATUCCTAGGAGATTATCACCAGAATTTTCCACC <u>ACGT</u> CACAAAGAAGTTAAAGAAGTTATUCCTAGGACAALLILAILINGI GUINGALAAACAAAGAAGAAGAAGAAAAGAAGAAAAAAAAAAA | ACATGGGGCAGTTACACACATTTTCTGCACCA <u>CGGG</u> CACAAAGAGTAACAAGTTATCCTAGGACTAAGAGTTATCCTAGGACAATCTCTATAGATATAGAAAAAAAA | ACATGGGGCAGTTACACACATTTTCTGCACATTTCCACC <u>ACGT</u> CACAAGAGTTATCCAGGGAGTTAGGAGAAALLICAAITAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | ACATGGGGCAGTTACACACATTTTCTGCACATTTCCACC <u>AGGG</u> CACAAAGAGTAAGAGTTATCCACAGACAALCAGAAAAAAAAAA | ACATGCGCAGTTACACACATTTTCTGCACATTTTCCACC <u>ACGT</u> CACAAAGAGTTAAGAGTTATCCTGAGAGATATCTCATTAGTGTAAGATAACAATCTATA
 | ACATGCGCAGTTACACACATTTCTGCACATTTCCACC <u>ACGT</u> CACAAAGAGTTAAGAGTTATCCCTAGGAAAATUTATTTTTTTTTT | ACATGOGCAGTTACACACTTTTCTGCACATTTCCACC <u>ACGT</u> CACAAAGAGCTAAGAGTTALCCTAGGACAALLICAITAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | ACATGCGCAGTTACCACATTTTCTGCACATTTCCACCACCACCACGAAAGAGCTAAAGAGTTATCCTTAGGAAAATULCATIAGTGTAAAAATULCATIAGTGAAAAAAA | ACATGCGCAGTTACACACATTTCTGCACATTTCCACCACGCACCACGGTCACGAGGTTATCCCTAGGACAATATCTCATTAGGACATAACATTACTGCAGTTACACACATTACTGCACTAGGACAGTTATCTGCACTACACACATACACACAGAGATAACAACAACAAAAAAAA | ACATGCGCAGTTACCACATTTTCTGCACATTTCCACCACGTCACAAGAGCTAAGAGTTATCCTAGAGATTACATCTCATTACTATATACATATATAT
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| CLO OLC OLC OLC OLC OLC OLC OLC OLC OLC | ACATGCGCAGTTACACACATTTCCACCACGTCACAAAGAGTTATCCACCAAAGAGTTATCCACAGGACAATTTCATTAGACATTTTCCACAAAAAAGAGTTATCCCAAAGAGTTATCCATTAGACAAAATTACCAAAAAAAA | IGITACACCACATITICTECACATUTTCCACCACGGGGCAAAAGAGGTAAGAGGTATCCCTAGGACAATCTATATGATAGGTAAAAAAAA | IGITACACCACTITITCTCCACATCTTCCACACACACACACA | IGITACACCACTITITCTCCACATCTTCCACACACACACACA
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 | IGITACACACATITICTGCACATTTCCACCACGGTCACAAAGAGTTATCCCTAGGACAATCTATATGTTAGTTA | IGITACACCACATITICTECACATTTTCCACCACATCACAAGAGGTAACAAGAGTAATCCCTAGGACAATCTATATGTAAGTATAAATCACAAAACATTCCACTAGGACAATCTATATGTAAGATAACAAAAAAAA | IGITACACACCATTTTCTCCACCACATTTCCACCACAAAAAACCTAAAAAA | IGITACACACATITICTGCACATITICCACCACGGGGGGGGGG | IGITACACACATITICTSCACATTTTCCACCACGTCACAAAGAGGTTATCCCTAGGACAATCTATATGATATATAT
 | IGITACACACATITICTCCACATCTTCCACACACACACACAC | IGITACACCACTITTCTCTCCACTACTACACAGGGTCACAAAGGGTTATCCCTAGGACAATCTCATTAGTTAG | IGPTRACACACTTYCTCCACCACGGGGGGGGGGGGGGGGGGGGGG | (GTTACACACATTTCTACACACACACACACACACACACACA | IGITACACACATITICTECACATITICCACCACATCACAAAGAGCTAAGAGTTATCCCTAGGACAATCTATATGTAGTAGTAAAAAACATACAT
 | IGITACACACACITITICTGCACATTTCCACCACATCACAAAAAGCTAAAAAGTTATCCCTAGGACAATCTATATGTAATCAATTCAATTAGTAATCAATTCCACTAGGACAATCTATTTTAGACAAAAAATCATTATTAGACAAAAATCATTATTAGACAAAAATCATTATTAGAAAAAATCATTATTTTAGAAAAAATCATTATTAGAAAAAAATCATTTTTAGCAAAAAAAA | IGITACACACATITYCTGCACATTTTCCACCACGGTCACAAAGAGTTATCCCTAGGACAATCTATATGTAGTTATCATTAGTCATTAGTTAG | IGITACACCACTITTCTCCACATTTTCTCCACCACGTCACAAAGAGTTATCCCTAGGACAATCTCATTAGTTAG | IGITACACCACTITICTCRCACATTTTCCACCACGGTCACAAAGAGTTATCCCTAGGACAATCTCATTAGTGTAGTAAAAAAAA | IGITACACACATITICTECACATTTTCCACCACGGTCACAAAGAGTTATCCCTAGGACAATCTATATGTTAGTTA
 | IGITACACACATITICTECACATITICCACCA <u>CGGT</u> CACAAAGAGCTAAGAGTTATCCCTAGGACAATCTATATGTAGTGTAATATATCACAAAAAATCATTACAATTACAATTACAAAAATTACCCAAAAAA | IGITACACACATITICTGCACATTTCCACCACGGTCACAAGAGCTAAGAGTTATCCCTAGGACAATCTATTTAGTGTAATTACACAAAACATACAACAACAACAAAAATTATCCACCA | ACHTGCGCAGTTACAACATTTTCTGCACTATTTCCACCACGTCACAAAGAGGTTATGCGCTAGGACAATTTCATTTAGTCATTTTCTCCACCACGTCACAAAAGGTTATTCACAAAAGAGGTCACAAAAGAGTTATTTTTTTT | ACATGCGCAGTTACACACATTTTCTGCACATTTTCTCCACGAGGCAAAAAAGTTATCCCTAGGACAATTCTATTAGGCACTTTTTCTCCCCACAAAAAGTTATCCCTAGGACAATTCTATTAGGCACATTCTTTTCTCCCACAAAAGTTTTTTCTCCAAAAAATTCTAGACAAAAAAAA | ACATGCGCAGTTACACACATTTCCACCACATTTCCACCACGTCACAAAAGAGTTATCCCCTAGGACAATCTCATTAGGTCATATTAGGTCACATTTACACACATTTTCCACCACGTCACAAAGAGTTATCCCCTAGGACAATCTCATTAGGTCACAAAAGTTACCCCACAAAAGTTATCCCTAGGACAAAAAAAA
 | Acargege Cagital Caracterity Coreca Cage Caraca Against Transcort Against Transcort | Acargedecagitaticrecacetriticeacetriticeacetriananditation Acargedecagitaticrecacetritical Acargedecagitaticrecacetritical 650 660 670 680 670 Total anima 630 640 650 660 700 690 700 Total animbox 730 740 750 760 790 800 Caadandaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa | ACATGCGCAGTTACAACAATTTCCACCAGGCACAAAAAAAA | ACATGCGCAGTTACACACATTTTCTGCACATTTTCCACCACGTCACAAAAAGTTAATCCTAGGACAATCTCATTAGTOTAAATAAAAAGTTAATCCTAGGACAATCTCATTAGTACATCATTATACACATCATCATTAAAAAAAGTTATACACAAAAAAAA | ACATGCGCAGTTACACACATTTTCTGCACCACGTCACAAAGAGGTAAGAGTTATCCCCTAGGACAATCTCATTAGGTGATAAGATAAAAGATTATCCCTAGGACAATCTCATTAGGTGACAATCTCATTAGGTGACACACCCTTTATAGACAAAAATTAGGTGACACAAAGATTATTTTGACAAAAATTAGACAAAAATTAGACAAAAATTAGACAAAAAAAA | ACATGCGCAGTTACACACATTTCCACCACGTCACAAAAAAGTTATCCACTAAAAAGTTATCCCTAGGACAATCTCATTAGTUTAATTATCATTATCATTATCATTATCATTATCATTATCATTATCATTATCATTATCATAAAATTATCCCTAAGAAGTTTATCACAAAATTATCCATAAAAATTATCCAAAAAATTATCAAAAAA
 | ACATGCGCAGTTACACACATTTCCACCAGGGCAGAGAGAG | ACATGCGCAGTTACAACATTTTCTGCACCAACGGTCAAAAAAGAGTTAAGAGTTATCCACGTAGAAAAAAAA | ACATGCGCAGTTACACACATTTCCACCACATTTCCACCACGCGCAAAAAAAA | ACATGCGCAGTTACACACATTTTCTGCACATTTCCACCACGTCACAAAGATTATACACATATACAGATATATACCAGAGATATATACATATATACATATACAATATACAAAAATATACAAAAAA
 | ACATGCGCAGTTACACACATTTTCTGCACATTTCCACCAGGCGTCACAAAGAGTTATCCACCTAAGAAGTTATTCCACAGGACAATTTTCTACACATTTTCCACCAGGACAATTTTTCACACACA | Acargegecargitacacacatitychecacatitycecaca <u>ceg</u> cacaaaggraaggraaggraaggraaggraaggraagg | ACATGCGCAGTTACACACATTTCCACCAGGTCACAAAGAGGTAAGAGTTATCCCTAGGACAATTCTATTAGTGTAAGATAAAGATTATCCACCAGGACAATTCTCATTAGTGTATAAACAATTATCACCAGGACAATTACCCAAGAGGACACCCAAAAAATTACCCAAGAGGACACCAAAAAATTACCAAAAAATTACCCAACACAAAAATTTTATAAAAAA | ACHTGCGCAGTTACAACATTTTCTGCACATTTTCCACCAGGTCACAAAGAGTTATCCCTAGGACAATCTCATTAGTGTAGAGTAAAAAAATTATCAAAAAAAA | ACATGCGCAGTTACAACATTTTCTGCACATTTTCCACCAGGGCAAAAAAAGTTATTCCCTAGGACAATCTCATTAGTGTAATTATTCACAGGACAATCTCATTAGTGTAATAAAAAAAA
 | ACATGCGCAGTTACACACATTTTCTCCACTCACACGCGCAAAAAAGATTATCCCTAGGACAATATTATCCCTAGGACAATTTTCTACACATTTTCCACTCACAAAAAAAA | ACATGCGCAGTTACACACATTTTCTCCACCACGTCACAAAAAGTTAAAAGTTATTCCACCAGGACAATTTTCCACCAGGACAATTTTCCACCAGGACAATTTTCCACCAGGACAAATTTTCACAAAAAAAA | ACATGCGCAGTTACACACATTTTCTCCACCACGTCACAAAAAAGTTATATCCACAAGAAAAAAGTTATATCCCTAGGACAATCTCATTAGGTGTAAAGATATATACACAAAAAAATTTTCCACCACAAAAAAAA | ACATGCGCAGTTACACACATTTCCACCACGTCACAAAAAAAGAGTAAAAGATTATCCACCACAAAAAAAA | ACATGCGCAGTTACACACATTTCCACCACGTCACAAAAAAAGGTAAAAAGTTATCCCCTAGGACAATTCTCATTTAGACATTTACACCACATTACATTTATCACACACA
 | ACATGCGCAGTTACACACATTTCCACC <u>ACGT</u> CACAAAGAGGTAAGAGGTTATCCCTAGGACAATTTCTATAGATGATTATCCACACAAAGAGGTAACCATTATATCCACCAGGACAATTTCCACCAAAAGAGGCAACAATTTCCACAAAAATTACCCAACAAAGATTATCACAAAAATTACCCAACAAAATTATATAAAAAAAA | ACATGCGCAGTTACAACAATTTTCTGCACCA <u>CGT</u> CACAAAGAGGTAAGAGTTATCCCTAGGACAATTTTCTAGCACATTTTCTCCACCA <u>CGT</u> CACAAAGAGGTAACCTTAAGAGGTAACCATAGATTACCAACAAAAATTACCCAACAAAAATTTATCAAGAAGCCTCTTTAATGACAAAAATAGGTGACAAAAAATTGCCCAACACAAAAATTACCCAACACAAAAATTACCCAACACAAAAATTACCCAACACAAAAATTACCCAACACAAAAATTACCCAACACAAAAATTACCCAACACAAAAATTACCCAACACAAAAATTACCCAACAA | ACATGCGCAGTTACAACAATTTCCACC <u>ACGT</u> CACAAAGAGGTAAGAGTTATCCCTAGGACAATCTCATTAGGTAAAAAAAA | ACATGCGCAGTTACAACATTTTCTGCACAAGAGGTAAGAGGTAAGAGGTAACAGGAAATTTACAACAATTTTCTACACAAAGAGGTAAGAGGTTAACATTTTAAGAGATTATTCACACAAAAGAGGTAAGAGGAAAATTAACAAAAATAAGAGGTAAAAAATAAGAGGTAAAAAATAAGAGAAAAATAAGAAAAATAAGAAAAATAAGAAAAATAAAAAA | ACATGCGCAGTTACACACATTTTCTGCACATTTTCCACCACGTCACAAAGAGGTAAGAGTTATCCCTAGGACAATTTTCTACACATTTTCTACACCATAGAAGTTATCCCTAGGACAATTTTCTACACATTATTCTACACATTATTCTACACATAGATAG
 | ACATGCGCAGTTACACACATTTTCTGCACATGCGCGCGCG | ACATGCGCAGTTACACACATTTCTCTCCACCACGTCACAAAGAGGTAAGAGTTATCCCCTAGGACAATTCTATTAGAGTTATCCACCAAAGAGGTAACCCTAGGACAATTTCTATTAGAGTTACCACAAAGGTAACCTTATTATCACAAAATTATCTGCCACATACAT | ACATGCGCAGTTACACACATTTCCACC <u>ACGT</u> CACAAAGAGGTAAGAGTTATCCACTAGGACAATCTCATTGGTAGATAGA | ACATGGGGCAGTTACACATTTTCTGCACA <u>CGT</u> CACAAAGAGTAACAGTTATCCACGAGACATTTTCTACACATTTTCTACACATTTTCTACACATTTTCTACACATTTTCTACACATTTTCTACACATTACATTTTATCACAAAAGACGTAAAAGACGTAAAAATTACCAAAAATTACACAAAAATTATCACAAAAATTTATCACAAAAAGAGAAAAATTACCAAAAATTACCAAAAATTTATCACAAAAAAA | ACATGCGCAGTTACACACATTTCCACCACGTCACAAAGAGTTATCCCTAGGACAATTTACAGACATATTATCATTAGATATATAT
 | ACATGCGCAGTTACACATTTTCTGCACATTTTCCACCAGGTCACAAAAAGTTATTCCACTAAGAATTATTAAAAATTAATAAAAAAAA | ACATGCGCAGTTACACACATTTCCACCAGGGTCACAAAGAGTTATCCCCTAGGACAATCTCATTAGATAAAAACTTAAAAAAAA | ACATGCGCAGTTACACAZATTTTCTGCACATTTCCACC <u>ACGT</u> CACAAAGAGTTATACAGGTTATACAGATATATCAGAAAAATTATACAATTATACAATTATACAATTATACAATTATACAATTATACAATTATACAAAAGATACATTATACAGAAAATTACACAAAAGATACATAC | ACATGCGCAGTTACACACATTTTCTGCACATTTCCACC <u>ACGT</u> CACAAAGAGTTATCCACCTAGGACAATCTCATTAGAGATATACACATCTAATTAGAGATATACATCAATTAAATAGATATAATACAATAAAAATACACATCAATTAATACAAATAAATAAAAATAAAAAA | ACATGCGCAGTTACACACATTTTCTGCACATTTCCACCACGTCACAAAGAGTTATCCCTAGGACAATCTCATTAGTGTAGACATATAA ACGT core prolaminox
 | ACATGGGGCAGTTACACACATTTTCTGCACATTTCCACCAGGTCACAAAGAGTTATCCCTAGGACAATCTCATTAGTGTAAGACATTAAA AGGT core prolaminbox | ACATGCGCAGTTACACACATTTCCACCAGGTCACAAAGAGTTATCCCTAGGACAATCTCATTAGAGATAAAAAAAA | ACATGCGCAGTTACACACATTTCCACCAGGTCACAAAGAGGTTATCCCTAGGACAATCTCATTAGAGATAACAACAAAAAAAGGTTATCCCTAGGACAATCTCATTAGAGATAACAAAAAAAA | ACATGCGCAGTTACACACATTTTCCACCACGTCACAAGAGGTAACAGGTATCCCTAGGACAATTTTCTACACACGTCACACATTTACACACATTTTCCACCACGTCACACACA | ACATGCGCAGTTTTTCTGCACATTTCCACC <u>ACGT</u> CACAAAGAGTTATCCCTAGGACAAUCTCATTAGAGAAAAAAAGAGTTATCCACCAGGACAATTTCTACACACATTTTCCACC <u>ACGT</u> CACAAAGAGATATCCACCAGGACAAUCTCATTAGAGAAAAAAAAAA
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 | ACATGGGGGAGTJACAGCACATTTTCTGCACG <u>CGTG</u> CACAAGAGTJAGAAGTJATTCCTGGGACAATTTTCTACACAGATTTTCTACACAGAGTJAGAGATJATCAATTAA
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Acgit ootootaataataa | acatgegecagtytichgegegeatyticegegegegegegegegegegegegegegegegegegeg | ACATGCGCAGTTACACACATTTTCTGCACATTTCCACC <u>ACGT</u>
CACAAAGAGTTATCCCTAGGACAATCTCATTAGAGTAAAAAAAA | acatgegeagtiacacacattttctgeacatttccacc <u>acst</u> cacaaggagetaagagttatccetaggacatttattagtgiaaataalumitea
acet ooke | ACATGCGCAGTTACACACATTTTCTGCACATTTCCACC <u>ACGT</u> CACAAAGAGTTATCCCTAGGAUAATCTCATTAGAGTAAGAATACACAATTAA | acatececaettacacacatttictecaccactticcac <u>acci</u> cacaagactaagattatccctaggacaatutlattagtegagaalalacateaeteaeteaeteaetea | ACATGCGCAGTTACACACATTTTCTGCACATTTCCACCACGTCACAAAGAGTTATTTTTTTT
 | acatgegeagttreacreatttttegeacattteeacc <u>aces</u> cacaaagagetaagagetatateeetaggaaateteattabietagaiacaiocai. | $ACATGCGCAGTTACCACACTTTTCTGCACATTTCCACC\overline{CACG1}CACAAAGAGTTAAGAGTTATCCCTAGGACAATCTCATTAGTGTAGATACACCATCATTAGT$ | ACATGCGCAGTTACACATTTTCTGCACATTTTCCACC <u>ACGT</u> CACAAAGAGCTAAGAGTTATCCTGGGACAATCTVATTAGTGTAGATATCACAATATAA | POPTION OF THE CONTINUE OF STREET OF | -1, =2, =3, 54, 55, 560 570 580 590 600 | -1, -2, -3, -4, -5,0 560 570 580 590 600 | 710 570 580 590 600 | 71 51 51 54 600 570 580 590 600 | -1, -1, -1, -1, -1, -1, -1, -1, -1, -1,
 | | 1.00 5.00 5.00 5.00 5.00 6.00 6.00 | 201 Cote 570 580 590 600 | ACGI core ACGI core 500 500 580 590 600 | ACGT core ACGT core ACGT core ACGT core ACGT core | ACGT core ACGT core | ACGT core | ACGT core
 | ACGT core | ACGT core | ACGT COZE | CGTGGGCTTCCAATCCTCCTCAAATTAAAGGGCCTTTTTAAAATTAGATTAGATTAGATTAGATTAGATTAGATACTTCTTTTAGATACAACTCTCTCAAATTAAAATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATTAGATAGATTAGA | CGTGGGCTTCCAATCCTCCTCAAATTAAAGTTAGATTAGATTAGTTGCCTTCTTCAGTCACCCAATAAAAGTACAAAACAACACAACAACACAACAACAACAACAACAACA | OGTGGGCTTCCAATCCTCCTAATTAAAGGGCCTTTTTTTAAAATTAGATAATTAGATATTTCTTTC
 | OBTEGGCTTCCAATCTCCTCAAATTAAAATTAGATAATTGCCTTCTTTCAGTCACCCCATAAAAGTACAAAACTACAACAACAACAACAACAACAACAACAACAA | OGTOGOGUTICCAATCCTCCAAATTAAAGGGCCCTTTTTAAAATTAGATAATTGCCTTCTTTCAGTCACCCCATAAAAGTACAAAACTACTACCAACAACAA ACGT core | 0GTGGGCTTCCAAATTAAAATTAAAATAGATAATTAGATTACCTTCTTTCAGTCACCCATAAAAGTACAAAACTACTACCAACAACAA
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 | GGTRACARCATTTTCTGCACATTTCCACCAGGGTCACAAAGGTTATCCCTAGGACAATCTCATTAGTTAG | (GYTRACHACATTTTCTCACCAGGGTCACAAAGGGTTATTCCTCTAGGACAATCTCATTAGTTAG | (GYTRACARCATTTTCTGCACTATTTCCACCAGGGTCACAAAGGTTATTCCTTAGGACAATCTCATTAGTTAG | (GYTRACARACHTTYCTGCACATTYCCACCAGGGTCACAAAGGTTATCCCTAGGACAATCYCATTAGTAGATACACATT (GYTRACACATTYCTGCACTAGGGTCACAAAGGTTATCCCTAGGACAATCYCATTAGTTAGATACATCATTAGTTAGATACATTACAT | (GYTRACARACHTTYCTGCACAATTYCCACCAGGGTCACAAAGGTTATCCCTAGGACAATCYCATTAGTAGATACACATT (GYTRACACATTYCTTATCACCAGGGTCACAAAGGTTATCCCTAGGACAATCYCATTAGTTAGATACATTCATTAGTTAGATACATTACAT
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 | GGTRACARACTITICTGCACATTTCCACCAGGGTCACAAAGGTTATCCCTAGGACAATCTCATTAGTAGATACACATTCATT | (GYTRACARACATTTTCTGCACTATTTCCACCAGGGTCACAAAGGTTATTCCTTAGGACAATCTCATTAGTTAG | (GYTRACARACTITYCTGCACAATTYCCACCAGGGTCACAAAGTTATCCCTAGGACAATCYCATTAGTTAGATACACCATT (GYTRACACATTYCTGCACAAAAATTAGTGACACAAAGTTATCCCTAGGACAATCYCATTAGTTAGATACATTACCATTACATTA | (GYTRACARACHTTYCTGCACCAGGGTCACAAAGGGTTATACCCTAGGACAATCTCATTAGTTAG | GOTTACACACTITTICTGCACATTTCCACCAGGGTCACAAAGGTTATCCCTAGGACAATCTCATTAGTGTAGATACACATCATCATTAGTGTAGATACACATCATCATTAGTGTAGATACACATCATTAGTAGATACATCATTAGTAGATACATTAGTAGATACATTAGTAGATACATTAGTAGATACATTAGTAGATAGA
 | GOTTACACACTITTICTGCACATTTCCACCAGGGTCACAAAGGTTATCCCTAGGACAATCTCATTAGTGTAGATACACATCATCATTAGTGTAGATACACATCATCATTAGTGTAGATACACATCATTAGTGTAGATACACATCATCATTAGTGTAGATACACATCATTAGTGTAGATACACATACAT | GOTTACACACTITICTGCACATTTCCACCAGGGTCACAAAGGTTATCCCCTAGGACAATCTCATTAGTGTAGATACACATTCATT | GGTRACARACTITICTECACATTTCCACCAGGGTCACAAAGGTTATCCCTAGGACAATCTCATTAGTAGATACACATTTCATTAGTAGATACACATTTCATTAGTAGATACACATTTCACATTTCCACATTTCATTAGTAGATACATTCATT | (GYTRACARACTITYCTGCACATTTCCACCAGGGTCACAAAGGGTTATCCCTAGGACAATCTCATTAGTTAG | GGTRACACACTITICTGCACATTTCCACCAGGGTCACAAAGGGTTATCCCTAGGACAATCTCATTAGTGTAGATACACATTCATT
 | GOTINGAGARATHICTGCACATTTCCACCAGGGTCACAAAGGTTATCCCTAGGACAATCTCATTAGTTAG | GOTING CONTINUED | ACATGCGCAGTTACACACATTTTCTGCACATTTTCCACCAGGGCACAAAAAGTTATTCCTCATTAGGGTAGATACATCATTAAGGATACATCATTAAGGATACATCATTAAGGATACATCATTAAGGATACATCATTAAGGATACATCATTAAGGATACATCATTAAGGATACATCATTAAGGATACATCATTAAGGATACATTAATCACAAAAATTAACACAAAAATTAACACAAAAATTAACACAAAAATTAAGACATTAATAAAAAAAA | ACATGCGCAGTTACAACATTTTCTGCACATTTTCTGCACGGCGCAAAAGAGGTAAGAGTTATCCCTAGGACAATTTTTTAGAGTAGATACATCATTAAAAATAAAAAAAA | ACATGGGGAGTHACACATTTTCTGCACATTTTCTACCAGGGCACAAAAAGTTATTCCCTAGGACAATCTCATTAGGGTAGATACATCATTAAAAAAAA | ACATGGGGAGTTACAACATTTTCTGCACATTTTCTACCAGGGCACAAAAAAGTTATTTCCCTTAGGACATTTTATGATAGATA
 | ACATGCGCAGTTACACACATTTTCTGCACATTTTCTACCACAGGTCACAAAGGTTAAGAGTTATTCCTGCATTAGAGTAGATACATCATTAAAAATAAAAAAATTCTACAAAGGTTAACAAAAAAAGGTTAACAAAAAGGTTAACAAAAAAAA | ACATGCGCAGTTACAACATTTTCTGCACAATTTTCTGCACAAAGAGCTAAGAGTTATTCCCTAGGACAATTTTTTTT | ACATGCGCAGTTACAACATTTTCTGCACATTTTCCACCAGGGCACACAAAAAGTTATTCCCTAGGACAATTTTTAGGATAAAAAAAA | ACATGCGCAGTTACAACATTTTCTGCACATTTCCACC <u>AGGG</u> CACAAAGAGCTAAAAGTTTTTCCCTAGGACAATTTTTTAATGATAGATA | ACATGCGCAGTTACAACATTTTCTGCACATTTTCTACCACGGGTCACAAAGAGCTAAAGAGTTATTCCCTTAGGATAGATA
 | ACATGCGCAGTTACACAATTTTCTGCACATTTTCTACCACAGGTCACAAAGAGCTAAGAGTTTTTCCTGGGGCAATTTTTTTT | ACATGCGCAGTTACACACATTTTCTGCACAGGTCACAAAGAGTTATTCCCTAGGACAATCTCATTAGTGTAGATACATCATTAA ACGT core prolaminox 640 650 660 7700 680 7700 680 7700 780 7700 770 | acatgegecaetaetrityctgecaetrityctgecaetritaeaagagctaacaaagagctaacaaagagctaacaagagcaarctaaagagcaarctaaaaaaataaagagctacaaaagaggagagagagagag | ACATGCGCAGTTACAACATTTTCTGCACATTTCCACCAGGCGCAAAAGGTTATTCCCTAGGACAATTTTTTATTAAAAAAAA | ACATGCGCAGTTACAACATTTTCTGCAGATTTCCACC <u>AGGT</u>
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 | acatgegecaetarcacaetitrictgecaeatitriceaecaegecaeaagaetraagaetraagaetarticeatitagaetaatracaeataaaaaaaaaaaaaaaaaaaaaaaaaaa | ACATGCGCAGTTACACACATTTTCTGCACATTTTCTACACGGGCACAAAAAGTTAAAAAGTTATTCCCTAGGACAATTTTCATTAAAAAATTTTAAAAAAAA | ACATGCGCAGTTACACAATTTCCACCAACGCGCACAAAAAGGTAAAAAGTTATCCCTAGGACAATTTCAATTAGTGTAGATAGA | ACATGCGCAGTTACACAATTTTCTGCACATTTTCCACCAGGTCACAAAGAGCTAAGAGTTATTCCCTAGGACAATCTCATTAGAGTAGATAGA | ACATGCGCAGTTACACAATTTTCTGCACATTTTCCACCAGGGCACAAAAAGTTATTCCCTAGGACAATTTAGTGTAGATAGA
 | ACATGCGCAGTTACACAATTTTCTGCACAAAGAGCTAAGAGTTATTCCCTAGGACAATTTGCTATTAGTGTAGATAGA | ACATGCGCAGTTACACACATTTTCTGCACCAGGGCACAAAGAGGTAAGAGTTATCCCTAGGGACAATCTCATTAGTGTAGATAGA | ACATGCGCAGTTACACACATTTTCTGCACCAGGGCACAAAGAGTAATGAGTTATCCCTAGGACAATCTCATTAGTGTAGATACATCCATTAA ACGT core prolaminbox | ACATGCGCAGTTTTCTTCCACCACTTTCCACCACGCTCAAAAGAGTTATCCCTAGGACAATCTCATTAGTGTAGATACATCCATTAA ACGT core prolaminbox | ACATGOGCAGTTTTCTGCACATTTCCACCACGGCACAAAGAGCTAAGAGTTATCCCTAGGGACAATCTCATTAGTGTAGATACATCCATTAAA ACGT core prolaminbox 610 650 670 680 690 700 TCTTTTATGACAAAATTAGTGACAAAAATTAGTGACAAAAATTAGTGACAAAAATTAGTGACAAAAATTAGTGACAAAAATTAGTGACAAAAATTAGTGACAAAAATTAGTAAAAATTAGTGACAAAAAATTAGTGACAAAAAAAA
 | ACATGCGCAGTTACACAATTTCCACCA <u>CGCGCACAAAAAAGCTAAAAGTTATCCCTAGGACAATTCCATTAGGAGTAGATACATCATATAA</u> AACATCATCATTAAAAATACATCAATAAAAAAAA | acargeselagiracacalatiticroelacacatricesece <u>aesi</u> cacaaagasetaagastariceetagsacaateteatitagigaaaatacatetaa
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	10 CTGCAGGCCAGGGAAA		110 ATAATGGACAATTAAA	210 TCCTATGTTAATTTTA	ACGT core	310 ACGTCATAGCATAGAT		410 ACCTGAAATGGGCTTT	510 TTTGCGGAAGCAATGG		610 GAAGGATAATCACTCC	710 GGCTTTAGCAGACCGT		810 TTGTTTCTTCACGC	txm_sta	910 TTCACAATCTCATCAT

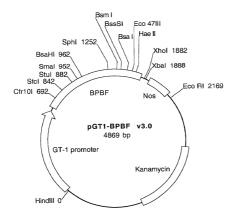


Fig. 11A

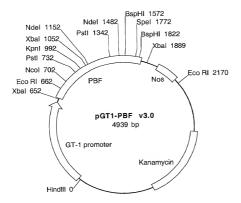


Fig. 11B

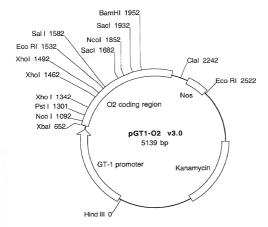


Fig. 11C

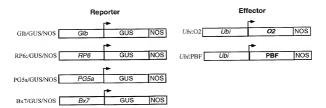


Fig. 12A

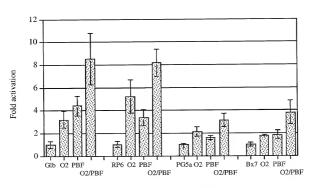


Fig. 12B



Fig. 13A

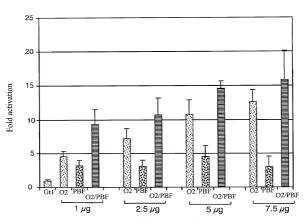


Fig. 13B

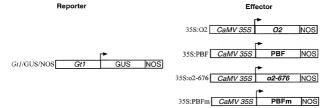
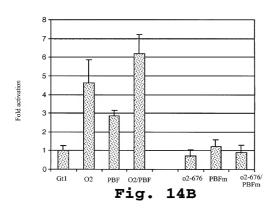


Fig. 14A



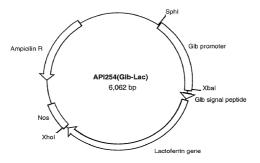


Fig. 15A

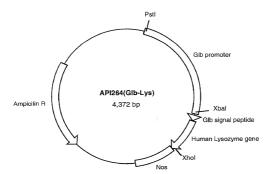


Fig. 15B

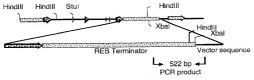


Fig. 16A

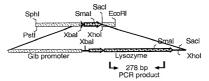


Fig. 16B

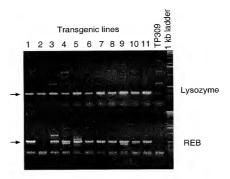


Fig. 16C

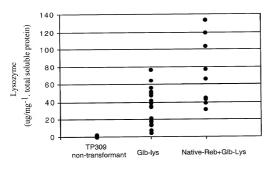


Fig. 17